

C. Kaufman

Re-run

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#12



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/601,582A

DATE: 10/03/2002

TIME: 15:12:21

Input Set : A:\20052YP.txt

Output Set: N:\CRF4\10032002\I601582A.raw

4 <110> APPLICANT: Liu, Qingyun
5 McDonald, Terrence
6 Bonnert, Timothy P.
7 Ng, Gordon
8 Kolakowski, Lee F., Jr.
9 Clark, Janet
10 Bonner, Tom I.
12 <120> TITLE OF INVENTION: NOVEL GABAB RECEPTOR DNA SEQUENCES
15 <130> FILE REFERENCE: 20052YP
17 <140> CURRENT APPLICATION NUMBER: 09/601,582A
18 <141> CURRENT FILING DATE: 2000-12-04
20 <150> PRIOR APPLICATION NUMBER: PCT/US99/02361
21 <151> PRIOR FILING DATE: 1999-02-03
23 <150> PRIOR APPLICATION NUMBER: 60/073,767
24 <151> PRIOR FILING DATE: 1998-02-05
26 <160> NUMBER OF SEQ ID NOS: 46
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 3480
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo Sapiens
35 <400> SEQUENCE: 1

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| 37 | tca | agagctcg | ctcccaaaaa | ttcccgccgt | gattgatccg | tcacgggcgc | ctccgctgcc | 120 |
| 38 | gcccggcccg | ccgcggccgt | tctgagccga | gcccggaa | ccccc | tagcccgaga | cggagccggg | 180 |
| 39 | gcccggggcc | gcccattgc | gccccggcccg | cgggaagacc | ttggcgcggg | gcggcggggcc | 240 | |
| 40 | ggggcaggcc | atgcggcccg | agtgagccgg | cggccgcagc | ccgcggccgc | gcatggcttc | 300 | |
| 41 | cccgccggagc | tccgggcagc | ccggggccgc | gcccgcgcg | ccaccgcgc | ccgcgcgcct | 360 | |
| 42 | gctactgcta | ctgctgctgc | cgtgctgc | gcctctggcg | cccggggcct | ggggctgggc | 420 | |
| 43 | gccccggcc | ccccggccgc | cggccagcag | ccgcgcgtc | tccatcatgg | gcctcatgcc | 480 | |
| 44 | gctcaccaag | gagggtggca | agggcagcat | cgggcgggt | gtgctccccc | ccgttggact | 540 | |
| 45 | ggccatcgag | cagatccgca | acgagtca | cctgcgc | ccccc | tacttcctcg | acctgcggct | 600 |
| 46 | ctatgacacg | gagtgcgaca | acgcaaaagg | gttggaa | agcc | ttctacatgt | caataaaaata | 660 |
| 47 | cggccgaac | cacttgatgg | tgtttggagg | cgtctgtcca | tccgtcacat | ccatcattgc | 720 | |
| 48 | agagtccctc | caaggctgga | atctggtgca | gttttcttt | gtgtcaacca | cgcctgttct | 780 | |
| 49 | agccgataag | aaaaaaatacc | cttatttctt | tcggaccgtc | ccatcagaca | atgcgggtaa | 840 | |
| 50 | tccagccatt | ctgaagtgc | tcaagcacta | ccagtggaa | cgcgtgggca | cgctgacgca | 900 | |
| 51 | agacgttcag | aggttctctg | aggtgcggaa | tgacctgact | ggagttctgt | atggcgagga | 960 | |
| 52 | cattgagatt | tcagacaccg | agagttctc | caacgatccc | tgtaccagt | tcaaaaagct | 1020 | |
| 53 | gaaggggaaat | gatgtgcgga | tcatccttg | ccagtttgc | cagaatatgg | cagaaaaagt | 1080 | |
| 54 | gttctgttgt | gcatacgagg | agaacatgt | tggtagtaaa | tatcagtgg | tcattccggg | 1140 | |
| 55 | ctggta | ccttcttgt | gggagcagg | gcacacggaa | gccaactcat | cccgctgcct | 1200 | |
| 56 | ccgaaagaat | ctgcttgctg | ccatggaggg | ctacattggc | gtggatttcg | agcccctgag | 1260 | |

ENTERED

p.6

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| 57 | ctccaaggcag | atcaagacca | tctcaggaaa | gactccacag | cagtatgaga | gagagtacaa | 1320 | | | | | | | | | |
| 58 | caacaaggcg | tcaggcgtgg | ggcccagcaa | gttccacggg | tacgcctacg | atggcatctg | 1380 | | | | | | | | | |
| 59 | ggtcatcgcc | aagacactgc | agagggccat | ggagacactg | catgccagca | gccggcacca | 1440 | | | | | | | | | |
| 60 | gcggatccag | gacttcaact | acacggacca | cacgctgggc | aggatcatcc | tcaatgccc | 1500 | | | | | | | | | |
| 61 | gaacgagacc | aacttctcg | gggtcacggg | tcaagttgt | ttccggaatg | gggagagaat | 1560 | | | | | | | | | |
| 62 | ggggaccatt | aaatttactc | aatttcaaga | cagcagggag | gtgaagggtgg | gagagtacaa | 1620 | | | | | | | | | |
| 63 | cgcgtgtggcc | gacacactgg | agatcatcaa | tgacaccatc | aggttccaag | gatccgaacc | 1680 | | | | | | | | | |
| 64 | acccaaaagac | aagaccatca | tcctggagca | gctgcggaaag | atctccctac | ctctctacag | 1740 | | | | | | | | | |
| 65 | catcctctct | gccctcacca | tcctcgggat | gatcatggcc | agtgcgtttc | tcttcttcaa | 1800 | | | | | | | | | |
| 66 | catcaagaac | cggaatcaga | agtcataaa | gatgtcgagt | ccatacatga | acaaccttat | 1860 | | | | | | | | | |
| 67 | catccttgg | gggatgtct | cctatgcttc | catatttetc | tttggccttg | atggatcctt | 1920 | | | | | | | | | |
| 68 | tgtctctgaa | aagacetttg | aaacactttg | caccgtcagg | acctggattc | tcaccgtggg | 1980 | | | | | | | | | |
| 69 | ctacacgacc | gcttttgggg | ccatgtttgc | aaagacctgg | agagtccacg | ccatcttcaa | 2040 | | | | | | | | | |
| 70 | aaatgtgaaa | atgaagaaga | agatcatcaa | ggaccagaaa | ctgcttgta | tcgtgggggg | 2100 | | | | | | | | | |
| 71 | catgctgctg | atcgacctgt | gtatcctgtat | ctgctggcag | gctgtggacc | ccctgcgaag | 2160 | | | | | | | | | |
| 72 | gacagtggag | aagtacagca | tggagccgga | cccagcagga | cgggatatact | ccatccgccc | 2220 | | | | | | | | | |
| 73 | tctcctggag | cactgtgaga | acacccatat | gaccatctgg | cttggcatacg | tctatgccta | 2280 | | | | | | | | | |
| 74 | caagggactt | ctcatgttgc | tcgggtgttt | tttagcttgg | gagacccgca | acgtcagcat | 2340 | | | | | | | | | |
| 75 | ccccgcactc | aacgacagca | agtagatcg | gatgagtgtc | tacaacgtgg | ggatcatgtg | 2400 | | | | | | | | | |
| 76 | catcatcg | gccgctgtct | ccttcctgac | ccgggaccag | ccaaatgtc | agttctgcata | 2460 | | | | | | | | | |
| 77 | cgtggctctg | gtcatcatct | tctgcagcac | catcaccctc | tgcctgttat | tcgtgccc | 2520 | | | | | | | | | |
| 78 | gctcatcacc | ctgagaacaa | acccagatgc | agcaacgcag | aacaggcgat | tccagttcac | 2580 | | | | | | | | | |
| 79 | tcagaatcag | aagaaagaag | attctaaaac | gtccacctcg | gtcaccagtg | tgaaccaagc | 2640 | | | | | | | | | |
| 80 | cagcacatcc | cgcctggagg | gcctacagtc | agaaaaaccat | cgccgcgaa | tgaagatcac | 2700 | | | | | | | | | |
| 81 | agagctggat | aaagacttgg | aagaggtcac | catgcagctg | caggacacac | cagaaaagac | 2760 | | | | | | | | | |
| 82 | cacctacatt | aaacagaacc | actaccaaga | gctcaatgac | atcctcaacc | tggaaaactt | 2820 | | | | | | | | | |
| 83 | cactgagagc | acagatggag | gaaaggccat | tttaaaaaat | cacctcgatc | aaaatcccc | 2880 | | | | | | | | | |
| 84 | gctacagtgg | aacacaacag | agccctctcg | aacatgaaaa | gatctatag | aagatataaa | 2940 | | | | | | | | | |
| 85 | ctctccagaa | cacatccagc | gtcggctgtc | cctccagctc | cccatectcc | accacgccta | 3000 | | | | | | | | | |
| 86 | cctcccatcc | atcggaggcg | tggacgcccag | ctgtgtcagc | ccctgcgtca | gccccaccgc | 3060 | | | | | | | | | |
| 87 | cagccccccgc | cacagacatg | tgccaccctc | cttcccgatc | atggtctcgg | gcctgttaagg | 3120 | | | | | | | | | |
| 88 | gtggggggcc | tggcccccgg | gcctcccccc | tgacagaacc | acactggc | gaggggtctg | 3180 | | | | | | | | | |
| 89 | ctgcagaaac | actgtcggt | ctggctgegg | agaagctgg | caccatggct | ggcctctcag | 3240 | | | | | | | | | |
| 90 | gaccactcg | atggcactca | ggtggacagg | acggggcagg | gggagacttg | gcacctgacc | 3300 | | | | | | | | | |
| 91 | tcgagccta | tttgtgaagt | ccttatttct | tcacaaagaa | gaggaacgga | aatgggacgt | 3360 | | | | | | | | | |
| 92 | cttccttaac | atctgcaaacc | aaggaggcgc | tggatatcr | aattccacca | cactggcggc | 3420 | | | | | | | | | |
| 93 | ccgcgcttgs | tcstaatcat | ggtcataact | gttccctgt | ttgaaattgt | tatccgc | 3480 | | | | | | | | | |
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| 97 | <212> | TYPE: | PRT | | | | | | | | | | | | | |
| 98 | <213> | ORGANISM: | Homo Sapiens | | | | | | | | | | | | | |
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| 101 | Met | Ala | Ser | Pro | Arg | Ser | Gly | Gln | Pro | Gly | Pro | Pro | Pro | Pro | | |
| 102 | 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| 103 | Pro | Pro | Pro | Pro | Ala | Arg | Leu | Leu | Leu | Leu | Leu | Leu | Pro | Leu | Leu | |
| 104 | | | | | | 20 | | | 25 | | | | | 30 | | |
| 105 | Leu | Pro | Leu | Ala | Pro | Gly | Ala | Trp | Gly | Trp | Ala | Arg | Gly | Ala | Pro | Arg |
| 106 | | | | | | 35 | | | 40 | | | | | 45 | | |
| 107 | Pro | Pro | Pro | Ser | Ser | Pro | Pro | Leu | Ser | Ile | Met | Gly | Leu | Met | Pro | Leu |

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| 108 | 50 | 55 | 60 |
| 109 | Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg Gly Val Leu Pro Ala | | |
| 110 | 65 | 70 | 75 |
| 111 | Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro | | 80 |
| 112 | 85 | 90 | 95 |
| 113 | Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu Cys Asp Asn Ala Lys | | |
| 114 | 100 | 105 | 110 |
| 115 | Gly Leu Lys Ala Phe Tyr Asp Ala Ile Lys Tyr Gly Pro Asn His Leu | | |
| 116 | 115 | 120 | 125 |
| 117 | Met Val Phe Gly Gly Val Cys Pro Ser Val Thr Ser Ile Ile Ala Glu | | |
| 118 | 130 | 135 | 140 |
| 119 | Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser Phe Ala Ala Thr Thr | | |
| 120 | 145 | 150 | 155 |
| 121 | Pro Val Leu Ala Asp Lys Lys Tyr Pro Tyr Phe Phe Arg Thr Val | | 160 |
| 122 | 165 | 170 | 175 |
| 123 | Pro Ser Asp Asn Ala Val Asn Pro Ala Ile Leu Lys Leu Leu Lys His | | |
| 124 | 180 | 185 | 190 |
| 125 | Tyr Gln Trp Lys Arg Val Gly Thr Leu Thr Gln Asp Val Gln Arg Phe | | |
| 126 | 195 | 200 | 205 |
| 127 | Ser Glu Val Arg Asn Asp Leu Thr Gly Val Leu Tyr Gly Glu Asp Ile | | |
| 128 | 210 | 215 | 220 |
| 129 | Glu Ile Ser Asp Thr Glu Ser Phe Ser Asn Asp Pro Cys Thr Ser Val | | |
| 130 | 225 | 230 | 235 |
| 131 | Lys Lys Leu Lys Gly Asn Asp Val Arg Ile Ile Leu Gly Gln Phe Asp | | 240 |
| 132 | 245 | 250 | 255 |
| 133 | Gln Asn Met Ala Ala Lys Val Phe Cys Cys Ala Tyr Glu Glu Asn Met | | |
| 134 | 260 | 265 | 270 |
| 135 | Tyr Gly Ser Lys Tyr Gln Trp Ile Ile Pro Gly Trp Tyr Glu Pro Ser | | |
| 136 | 275 | 280 | 285 |
| 137 | Trp Trp Glu Gln Val His Thr Glu Ala Asn Ser Ser Arg Cys Leu Arg | | |
| 138 | 290 | 295 | 300 |
| 139 | Lys Asn Leu Leu Ala Ala Met Glu Gly Tyr Ile Gly Val Asp Phe Glu | | |
| 140 | 305 | 310 | 315 |
| 141 | Pro Leu Ser Ser Lys Gln Ile Lys Thr Ile Ser Gly Lys Thr Pro Gln | | 320 |
| 142 | 325 | 330 | 335 |
| 143 | Gln Tyr Glu Arg Glu Tyr Asn Asn Lys Arg Ser Gly Val Gly Pro Ser | | |
| 144 | 340 | 345 | 350 |
| 145 | Lys Phe His Gly Tyr Ala Tyr Asp Gly Ile Trp Val Ile Ala Lys Thr | | |
| 146 | 355 | 360 | 365 |
| 147 | Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg | | |
| 148 | 370 | 375 | 380 |
| 149 | Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu | | |
| 150 | 385 | 390 | 395 |
| 151 | Asn Ala Met Asn Glu Thr Asn Phe Phe Gly Val Thr Gly Gln Val Val | | 400 |
| 152 | 405 | 410 | 415 |
| 153 | Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln | | |
| 154 | 420 | 425 | 430 |
| 155 | Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr | | |
| 156 | 435 | 440 | 445 |

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157 Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln Gly Ser Glu Pro Pro
158 450 455 460
159 Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg Lys Ile Ser Leu Pro
160 465 470 475 480
161 Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala
162 485 490 495
163 Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
164 500 505 510
165 Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
166 515 520 525
167 Leu Ser Tyr Ala Ser Ile Phe Leu Phe Gly Leu Asp Gly Ser Phe Val
168 530 535 540
169 Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val Arg Thr Trp Ile Leu
170 545 550 555 560
171 Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met Phe Ala Lys Thr Trp
172 565 570 575
173 Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Ile Ile
174 580 585 590
175 Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
176 595 600 605
177 Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr
178 610 615 620
179 Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
180 625 630 635 640
181 Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp
182 645 650 655
183 Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys
184 660 665 670
185 Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile Pro Ala Leu Asn Asp
186 675 680 685
187 Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val Gly Ile Met Cys Ile
188 690 695 700
189 Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp Gln Pro Asn Val Gln
190 705 710 715 720
191 Phe Cys Ile Val Ala Leu Val Ile Ile Phe Cys Ser Thr Ile Thr Leu
192 725 730 735
193 Cys Leu Val Phe Val Pro Lys Leu Ile Thr Leu Arg Thr Asn Pro Asp
194 740 745 750
195 Ala Ala Thr Gln Asn Arg Arg Phe Gln Phe Thr Gln Asn Gln Lys Lys
196 755 760 765
197 Glu Asp Ser Lys Thr Ser Thr Ser Val Thr Ser Val Asn Gln Ala Ser
198 770 775 780
199 Thr Ser Arg Leu Glu Gly Leu Gln Ser Glu Asn His Arg Leu Arg Met
200 785 790 795 800
201 Lys Ile Thr Glu Leu Asp Lys Asp Leu Glu Glu Val Thr Met Gln Leu
202 805 810 815
203 Gln Asp Thr Pro Glu Lys Thr Tyr Ile Lys Gln Asn His Tyr Gln
204 820 825 830
205 Glu Leu Asn Asp Ile Leu Asn Leu Gly Asn Phe Thr Glu Ser Thr Asp

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|-----|------------|------------|--------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 206 | 835 | 840 | 845 | | | | | | | | | | | | | | |
| 207 | Gly | Gly | Lys | Ala | Ile | Leu | Lys | Asn | His | Leu | Asp | Gln | Asn | Pro | Gln | Leu | |
| 208 | 850 | | 855 | | | | 860 | | | | | | | | | | |
| 209 | Gln | Trp | Asn | Thr | Thr | Glu | Pro | Ser | Arg | Thr | Cys | Lys | Asp | Pro | Ile | Glu | |
| 210 | 865 | | 870 | | | 875 | | | 880 | | | | | | | | |
| 211 | Asp | Ile | Asn | Ser | Pro | Glu | His | Ile | Gln | Arg | Arg | Leu | Ser | Leu | Gln | Leu | |
| 212 | | | | | 885 | | | 890 | | | 895 | | | | | | |
| 213 | Pro | Ile | Leu | His | His | Ala | Tyr | Leu | Pro | Ser | Ile | Gly | Gly | Val | Asp | Ala | |
| 214 | | | | | 900 | | | 905 | | | 910 | | | | | | |
| 215 | Ser | Cys | Val | Ser | Pro | Cys | Val | Ser | Pro | Thr | Ala | Ser | Pro | Arg | His | Arg | |
| 216 | | 915 | | | 920 | | | 925 | | | | | | | | | |
| 217 | His | Val | Pro | Pro | Ser | Phe | Arg | Val | Met | Val | Ser | Gly | Leu | | | | |
| 218 | | 930 | | | 935 | | | 940 | | | | | | | | | |
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| 222 | <212> | TYPE: | DNA | | | | | | | | | | | | | | |
| 223 | <213> | ORGANISM: | Homo Sapiens | | | | | | | | | | | | | | |
| 225 | <400> | SEQUENCE: | 3 | | | | | | | | | | | | | | |
| 226 | ccgttctgag | ccgagccg | | | | | | | | | | | | | | 18 | |
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| 237 | <211> | LENGTH: | 20 | | | | | | | | | | | | | | |
| 238 | <212> | TYPE: | DNA | | | | | | | | | | | | | | |
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| 242 | ggatgtatca | tggccagtgc | | | | | | | | | | | | | | 20 | |
| 244 | <210> | SEQ | ID | NO: | 6 | | | | | | | | | | | | |
| 245 | <211> | LENGTH: | 20 | | | | | | | | | | | | | | |
| 246 | <212> | TYPE: | DNA | | | | | | | | | | | | | | |
| 247 | <213> | ORGANISM: | Homo Sapiens | | | | | | | | | | | | | | |
| 249 | <400> | SEQUENCE: | 6 | | | | | | | | | | | | | 20 | |
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| 252 | <210> | SEQ | ID | NO: | 7 | | | | | | | | | | | | |
| 253 | <211> | LENGTH: | 19 | | | | | | | | | | | | | | |
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| 266 | ttggttcaca | ctggtgaccg | a | | | | | | | | | | | | | 21 | |

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/03/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 1992